

Package ‘scToppR’

May 20, 2026

Title API Wrapper for ToppGene

Version 1.1.0

Description scToppR provides an easy-to-use API wrapper for the ToppGene web platform, used for gene ontology and functional enrichment research. The package also integrates visualization tools, making it a convenient tool directly connecting ToppGene to code-based workflows in R. The tool can also easily save results into different formats.

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Imports dplyr, forcats, ggplot2, stringr, openxlsx, viridis,
patchwork, utils, httr2

Depends R (>= 4.5.0)

LazyData false

Suggests airway, BiocStyle, curl, DESeq2, knitr, rmarkdown, S4Vectors,
SingleCellExperiment, SummarizedExperiment, testthat (>= 3.0.0)

VignetteBuilder knitr

biocViews Pathways, SingleCell

BugReports <https://github.com/BioinformaticsMUSC/scToppR>

URL <https://github.com/BioinformaticsMUSC/scToppR>

Config/testthat/edition 3

git_url <https://git.bioconductor.org/packages/scToppR>

git_branch devel

git_last_commit c7f5306

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-19

Author Bryan Granger [aut, cre] (ORCID:
<<https://orcid.org/0009-0008-6663-3755>>)

Maintainer Bryan Granger <grangerb@musc.edu>

Contents

scToppR-package	2
addToppData	3
addToppData	4
get_Entrez	5
get_ToppCats	5
ifnb.de	6
ifnb.markers.df	6
ifnb.markers.list.CD8T	7
pbmc.markers	8
toppBalloon	8
toppdata.airway	9
toppdata.ifnb	10
toppdata.pbmc	11
toppFun	12
toppPlot	14
toppSave	15
Index	17

scToppR-package

scToppR: API Wrapper for ToppGene

Description

scToppR provides an easy-to-use API wrapper for the ToppGene web platform, used for gene ontology and functional enrichment research. The package also integrates visualization tools, making it a convenient tool directly connecting ToppGene to code-based workflows in R. The tool can also easily save results into different formats.

Author(s)

Maintainer: Bryan Granger <grangerb@musc.edu> ([ORCID](#))

See Also

Useful links:

- <https://github.com/BioinformaticsMUSC/scToppR>
- Report bugs at <https://github.com/BioinformaticsMUSC/scToppR>

addToppData	<i>Add toppData results to SingleCellExperiment or SummarizedExperiment metadata</i>
-------------	--

Description

A convenience function to store `toppData` enrichment results in the metadata slot of a `SingleCellExperiment` or `SummarizedExperiment` object. Results are stored directly under the specified slot name, with optional analysis parameters stored in a separate `slot_name_params` slot.

Usage

```
addToppData(  
  sce,  
  toppData_results,  
  slot_name = "toppData",  
  include_params = TRUE  
)
```

Arguments

<code>sce</code>	A <code>SingleCellExperiment</code> or <code>SummarizedExperiment</code> object
<code>toppData_results</code>	A <code>data.frame</code> of <code>toppData</code> results from <code>toppFun()</code>
<code>slot_name</code>	Name for the metadata slot (default: "toppData")
<code>include_params</code>	Logical, whether to include analysis parameters and timestamp in a separate <code>slot_name_params</code> slot (default: TRUE)

Value

`SingleCellExperiment` or `SummarizedExperiment` object with `toppData` stored in metadata

Examples

```
library(airway)  
data("airway") # example SummarizedExperiment object  
data("toppdata.airway") # example toppData results  
se_with_topp <- addToppData(airway, toppdata.airway)  
  
# Access results directly  
topp_results <- S4Vectors::metadata(se_with_topp)$toppData  
  
# Access analysis parameters (if include_params = TRUE)  
topp_params <- S4Vectors::metadata(se_with_topp)$toppData_params
```

addToppData	<i>Add toppData results to SingleCellExperiment or SummarizedExperiment metadata</i>
-------------	--

Description

A convenience function to store `toppData` enrichment results in the metadata slot of a `SingleCellExperiment` or `SummarizedExperiment` object. Results are stored directly under the specified slot name, with optional analysis parameters stored in a separate `slot_name_params` slot.

Usage

```
addToppData(  
  sce,  
  toppData_results,  
  slot_name = "toppData",  
  include_params = TRUE  
)
```

Arguments

<code>sce</code>	A <code>SingleCellExperiment</code> or <code>SummarizedExperiment</code> object
<code>toppData_results</code>	A <code>data.frame</code> of <code>toppData</code> results from <code>toppFun()</code>
<code>slot_name</code>	Name for the metadata slot (default: "toppData")
<code>include_params</code>	Logical, whether to include analysis parameters and timestamp in a separate <code>slot_name_params</code> slot (default: TRUE)

Value

`SingleCellExperiment` or `SummarizedExperiment` object with `toppData` stored in metadata

Examples

```
library(airway)  
data("airway") # example SummarizedExperiment object  
data("toppdata.airway") # example toppData results  
se_with_topp <- addToppData(airway, toppdata.airway)  
  
# Access results directly  
topp_results <- S4Vectors::metadata(se_with_topp)$toppData  
  
# Access analysis parameters (if include_params = TRUE)  
topp_params <- S4Vectors::metadata(se_with_topp)$toppData_params
```

get_Entrez	<i>Convert genes into Entrez format</i>
------------	---

Description

Convert genes into Entrez format

Usage

```
get_Entrez(genes)
```

Arguments

genes A list of genes

Value

a vector of genes in Entrez format

Examples

```
get_Entrez(genes = c("IFNG", "FOXP3"))
```

get_TopCats	<i>Get a vector of ToppFun categories</i>
-------------	---

Description

Get a vector of ToppFun categories

Usage

```
get_TopCats()
```

Value

a vector

Examples

```
get_TopCats()
```

ifnb.de

IFNB DE results

Description

A dataframe of differentially expressed genes generated using the FindMarkers function for each cluster from the Kang 2018 IFNB dataset Created using the IFNB dataset from the SeuratData package

Usage

```
data("ifnb.de")
```

Format

A dataframe with 92,860 rows and 7 columns

p_val P values

avg_log2FC avg log 2 fc values

pct.1 percentage of cells expressing gene in group 1

pct.2 percentage of cells expressing gene in group 2

p_val_adj adjusted p-value (FDR)

cluster cell group name

gene gene name

Source

<https://www.nature.com/articles/nbt.4042>

ifnb.markers.df*IFNB Marker DF*

Description

A dataframe of 100 top markers for each class in 'seurat_annotatons' column using presto::wilcoxauc() and presto::top_markers() Created using the IFNB dataset from the SeuratData package

Usage

```
data("ifnb.markers.df")
```

Format

A dataframe with 100 rows and 14 columns

rank rank of marker

B cell group name

B Activated cell group name

CD14 Mono cell group name

CD16 Mono cell group name

CD4 Memory T cell group name

CD4 Naive T cell group name

CD8 T cell group name

DC cell group name

Eryth cell group name

Mk cell group name

CNK cell group name

pDC cell group name

T activated cell group name

Source

<https://www.nature.com/articles/nbt.4042>

Kang HM, Subramaniam M, Targ S, et al. Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nat Biotechnol. 2018;36(1):89-94. doi:10.1038/nbt.4042

ifnb.markers.list.CD8T

IFNB Marker DF

Description

A list of the 100 top markers for CD8 T cells in ifnb dataset using `presto::wilcoxauc()` and `presto::top_markers()`
Created using the IFNB dataset from the SeuratData package

Usage

```
data("ifnb.markers.list.CD8T")
```

Format

A character vector with 100 genes

ifnb.markers.list.CD8T rank of marker

Source

<https://www.nature.com/articles/nbt.4042>

Kang HM, Subramaniam M, Targ S, et al. Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nat Biotechnol. 2018;36(1):89-94. doi:10.1038/nbt.4042

pbmc.markers

PBMC markers

Description

A dataframe of marker genes generated using the FindMarkers function for each cluster from the PBMC 3k dataset

Usage

```
data("pbmc.markers")
```

Format

A dataframe with 11,629 rows and 7 columns

p_val P values

avg_log2FC avg log 2 fc values

pct.1 percentage of cells expressing gene in group 1

pct.2 percentage of cells expressing gene in group 2

p_val_adj adjusted p-value (FDR)

cluster cell group name

gene gene name

Source

10X Genomics PBMC 3k dataset. Available from <https://www.10xgenomics.com/resources/datasets/>. Analysis following Seurat PBMC tutorial: https://satijalab.org/seurat/articles/pbmc3k_tutorial.html

toppBalloon

Create a balloon plot from toppdata results

Description

This function creates balloon plots from ToppGene enrichment results. It accepts either a data.frame with toppData results, or a SummarizedExperiment/SingleCellExperiment object with toppData stored in the metadata.

Usage

```
toppBalloon(  
  toppData,  
  categories = NULL,  
  balloons = 3,  
  x_axis_text_size = 6,  
  cluster_col = "Cluster",  
  filename = "toppBalloon",
```

```

    save = FALSE,
    save_dir = tempdir(),
    height = 6,
    width = 8,
    slot_name = "toppData",
    ...
  )

```

Arguments

toppData	A toppData results dataframe, SummarizedExperiment, or SingleCellExperiment object
categories	The topp categories to plot
balloons	Number of balloons per group to plot
x_axis_text_size	Size of the text on the x axis
cluster_col	The column name for clusters (default: "Cluster")
filename	Filename of the saved balloon plot
save	Save the balloon plot if TRUE
save_dir	Directory to save the balloon plot
height	Height of the saved balloon plot
width	Width of the saved balloon plot
slot_name	For SE/SCE objects, the metadata slot name containing toppData (default: "toppData")
...	Additional parameters for future use

Value

ggplot object or list of ggplot objects

Examples

```

data("toppdata.pbmc")

# With dataframe
toppBalloon(toppdata.pbmc, balloons = 3, save = FALSE)

# With SummarizedExperiment (if toppData stored in metadata)
# toppBalloon(se_object, categories = "GeneOntologyMolecularFunction")

```

toppdata.airway

toppData example using the airway dataset results

Description

A dataframe of of sample toppData results created from the ifnb.de dataset using the toppFun() function

Usage

```
data("toppdata.airway")
```

Format

A dataframe with 902 rows and 14 columns

Category ToppGene category

ID ToppGene Term ID

Name ToppGene Term Name

PValue P value

QValueFDRBH adjusted p-value (FDR)

QValueFDRBY adjusted p-value (BY)

QValueBonferroni adjusted p-value (Bonferroni)

TotalGenes Total genes in background

GenesInTerm Genes in ToppGene Term

GenesInQuery Genes in submitted query

GenesInTermQuery Intersection of genes in Term and in Query

Source ToppGene result source

URL ToppGene associated URL

Cluster cell group name

Source

<https://toppgene.cchmc.org>

Generated using ToppGene API (<https://toppgene.cchmc.org/>). Chen J, Bardes EE, Aronow BJ, Jegga AG. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. *Nucleic Acids Res.* 2009;37(Web Server issue):W305-11. doi: 10.1093/nar/gkp427.

Himes, E. B, Jiang, X., Wagner, P., Hu, R., Wang, Q., Klanderma, B., Whitaker, M. R, Duan, Q., Lasky-Su, J., Nikolos, C., Jester, W., Johnson, M., Panettieri, A. R, Tantisira, G. K, Weiss, T. S, Lu, Q. (2014). "RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells." *PLoS ONE*, 9(6), e99625. <http://www.ncbi.nlm.nih.gov/pubmed/24926665>.

<https://www.bioconductor.org/packages/release/data/experiment/html/airway.html>

toppdata.ifnb

toppData example for ifnb.de

Description

A dataframe of of sample toppData results created from the ifnb.de dataset using the toppFun() function

Usage

```
data("toppdata.ifnb")
```

Format

A dataframe with 12,227 rows and 14 columns

Category ToppGene category

ID ToppGene Term ID

Name ToppGene Term Name

PValue P value

QValueFDRBH adjusted p-value (FDR)

QValueFDRBY adjusted p-value (BY)

QValueBonferroni adjusted p-value (Bonferroni)

TotalGenes Total genes in background

GenesInTerm Genes in ToppGene Term

GenesInQuery Genes in submitted query

GenesInTermQuery Intersection of genes in Term and in Query

Source ToppGene result source

URL ToppGene associated URL

Cluster cell group name

Source

Generated using ToppGene API (<https://toppgene.cchmc.org/>). Chen J, Bardes EE, Aronow BJ, Jegga AG. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. Nucleic Acids Res. 2009;37(Web Server issue):W305-11. doi: 10.1093/nar/gkp427.

<https://toppgene.cchmc.org>

Kang HM, Subramaniam M, Targ S, et al. Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nat Biotechnol. 2018;36(1):89-94. doi:10.1038/nbt.4042

toppdata.pbmc

toppData example

Description

A dataframe of of sample toppData results created from the pbmc.markers dataset using the topp-Fun() function

Usage

```
data("toppdata.pbmc")
```

Format

A dataframe with 8,550 rows and 14 columns

Category ToppGene category

ID ToppGene Term ID

Name ToppGene Term Name

PValue P value

QValueFDRBH adjusted p-value (FDR)

QValueFDRBY adjusted p-value (BY)

QValueBonferroni adjusted p-value (Bonferroni)

TotalGenes Total genes in background

GenesInTerm Genes in ToppGene Term

GenesInQuery Genes in submitted query

GenesInTermQuery Intersection of genes in Term and in Query

Source ToppGene result source

URL ToppGene associated URL

Cluster cell group name

Source

<https://toppgene.cchmc.org>

Generated using ToppGene API (<https://toppgene.cchmc.org/>). Chen J, Bardes EE, Aronow BJ, Jegga AG. ToppGene Suite for gene list enrichment analysis and candidate gene prioritization. *Nucleic Acids Res.* 2009;37(Web Server issue):W305-11. doi: 10.1093/nar/gkp427.

10X Genomics PBMC 3k dataset. Available from <https://www.10xgenomics.com/resources/datasets/>. Analysis following Seurat PBMC tutorial: https://satijalab.org/seurat/articles/pbmc3k_tutorial.html

toppFun

Get results from ToppFun

Description

The `toppFun()` function takes a `data.frame` or other tabular data structure and selects genes to use in querying ToppGene.

Usage

```
toppFun(
  input_data,
  type = "degs",
  topp_categories = NULL,
  cluster_col = "cluster",
  gene_col = "gene",
  p_val_col = "adj_p_val_col",
  logFC_col = "avg_logFC",
```

```

direction_mode = "all",
num_genes = 1000,
pval_cutoff = 0.5,
fc_cutoff = 0,
fc_filter = "ALL",
clusters = NULL,
correction = "FDR",
key_type = "SYMBOL",
min_genes = 2,
max_genes = 1500,
max_results = 50,
verbose = TRUE
)

```

Arguments

input_data	A vector of markers or dataframe with columns as cluster labels
type	One of c("degs", "marker_list", or "marker_df). If "degs" is selected, the input_data is assumed to be a data.frame with logfoldchange, pvalue, and gene name columns. If "marker_list" is selected, input_data is assumed to be a list of genes with no other stats, and any thresholds pertaining to "degs" will be ignored. If "marker_df" is selected, the input_data is assumed to be a data.frame with columns as clusters/celltypes, and entries are lists of markers.
topp_categories	A string or vector with specific toppfun categories for the query
cluster_col	Column name for the groups of cells (e.g. cluster or celltype)
gene_col	Column name for genes (e.g. gene or feature)
p_val_col	Column name for the p-value or adjusted p-value (preferred)
logFC_col	Column name for the avg log FC column
direction_mode	One of c("all", "split"). Whether to use all genes in the pathway analysis, or to split by up and down regulated genes
num_genes	Number of genes per group to use for toppGene query
pval_cutoff	(adjusted) P-value cutoff for filtering differentially expressed genes
fc_cutoff	Avg log fold change cutoff for filtering differentially expressed genes
fc_filter	Include "ALL" genes, or only "UPREG" or "DOWNREG" for each cluster
clusters	Which clusters to include in toppGene query
correction	P-value correction method ("FDR" is "BH")
key_type	Gene name format
min_genes	Minimum number of genes to match in a query
max_genes	Maximum number of genes to match in a query
max_results	Maximum number of results per cluster
verbose	Verbosity setting, TRUE or FALSE

Details

The use of data from ToppGene is governed by their Terms of Use: <https://toppgene.cchmc.org/navigation/termsfuse.jsp>

Value

data.frame

Examples

```
data("ifnb.de")
toppData <- toppFun(ifnb.de,
  topp_categories = NULL,
  cluster_col = "celltype",
  gene_col = "gene",
  p_val_col = "p_val_adj",
  logFC_col = "avg_log2FC"
)
```

toppPlot

*Create a dotplot from toppdata results***Description**

This function creates dotplots from ToppGene enrichment results. It accepts either a data.frame with toppData results, or a SummarizedExperiment/SingleCellExperiment object with toppData stored in the metadata.

Usage

```
toppPlot(
  toppData,
  category = NULL,
  clusters = NULL,
  cluster_col = "Cluster",
  p_val_adj = "QValueFDRBH",
  p_val_display = "FDR_BH",
  num_terms = 10,
  save = FALSE,
  save_dir = tempdir(),
  width = 8,
  height = 6,
  file_prefix = "toppPlot",
  combine = FALSE,
  ncols = 2,
  y_axis_text_size = 10,
  slot_name = "toppData",
  ...
)
```

Arguments

toppData	A toppData results dataframe, SummarizedExperiment, or SingleCellExperiment object
category	The topp categories to plot
clusters	The cluster(s) to plot

cluster_col	The column name for clusters (default: "Cluster")
p_val_adj	The P-value correction method: "BH", "Bonferroni", "BY", or "none"
p_val_display	If "log", display the p-value in terms of $-\log_{10}(p_value)$
num_terms	The number of terms from the toppData results to be plotted, per cluster
save	Whether to save the file automatically
save_dir	Directory to save file
width	width of the saved file (inches)
height	height of the saved file (inches)
file_prefix	file prefix if saving the plot - the cluster name is also added automatically
combine	If TRUE and multiple clusters selected, return a patchwork object of all plots; if FALSE return list of plots
ncols	If patchwork element returned, number of columns for subplots
y_axis_text_size	Size of the Y axis text - for certain categories, it's helpful to decrease this
slot_name	For SE/SCE objects, the metadata slot name containing toppData (default: "toppData")
...	Additional parameters for future use

Value

ggplot object or list of ggplot objects

Examples

```
data("toppdata.pbmc")

# With data.frame
toppPlot(toppdata.pbmc,
  category = "GeneOntologyMolecularFunction",
  clusters = 0,
  save = FALSE
)

# With SummarizedExperiment (if toppData stored in metadata)
# toppPlot(se_object, category = "GeneOntologyMolecularFunction")
```

toppSave

Save toppData results (optionally) split by celltype/cluster

Description

Save toppData results (optionally) split by celltype/cluster

Usage

```
toppSave(  
  toppData,  
  filename = "toppData_results",  
  save_dir = NULL,  
  split = TRUE,  
  format = "xlsx",  
  cluster_col = "Cluster",  
  verbose = TRUE  
)
```

Arguments

toppData	Results from toppFun as a dataframe
filename	filename prefix for each split file
save_dir	the directory to save files
split	Boolean, whether to split the dataframe by celltype/cluster
format	Saved file format, one of c("xlsx", "csv", "tsv")
cluster_col	Column name for the groups of cells (e.g. cluster or celltype), usually "Cluster"
verbose	Verbosity setting, TRUE or FALSE

Value

A saved file

Examples

```
data("toppdata.ifnb")  
toppSave(toppdata.ifnb,  
  filename = "toppFun_results",  
  save_dir = tempdir(),  
  split = TRUE,  
  format = "xlsx")
```

Index

* datasets

- ifnb.de, [6](#)
- ifnb.markers.df, [6](#)
- ifnb.markers.list.CD8T, [7](#)
- pbmc.markers, [8](#)
- toppdata.airway, [9](#)
- toppdata.ifnb, [10](#)
- toppdata.pbmc, [11](#)

* internal

- scToppR-package, [2](#)

[addToppData](#), [3](#), [4](#)

[get_Entrez](#), [5](#)

[get_ToppCats](#), [5](#)

[ifnb.de](#), [6](#)

[ifnb.markers.df](#), [6](#)

[ifnb.markers.list.CD8T](#), [7](#)

[pbmc.markers](#), [8](#)

[scToppR \(scToppR-package\)](#), [2](#)

[scToppR-package](#), [2](#)

[toppBalloon](#), [8](#)

[toppdata.airway](#), [9](#)

[toppdata.ifnb](#), [10](#)

[toppdata.pbmc](#), [11](#)

[toppFun](#), [12](#)

[toppPlot](#), [14](#)

[toppSave](#), [15](#)